UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/783,807	02/20/2004	Tetsuo Shibuya	JP920030020US1	7767

7590 11/28/2007

William E. Lewis
Ryan, Mason & Lewis, LLP
90 Forest Avenue
Locust Valley, NY 11560

EXAMINER	
SMITH, CAROLYN L	

ART UNIT	PAPER NUMBER
1631	

MAIL DATE	DELIVERY MODE
11/28/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/783,807	SHIBUYA, TETSUO	
	Examiner	Art Unit	
	Carolyn L. Smith	1631	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *13 September 2007*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-19* is/are pending in the application.

4a) Of the above claim(s) *4-7,10-12,15,16,18 and 19* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-3, 8-9, 13-14, 17* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

A request for continued examination under 37 CFR 1.114, including the fee set forth in 37 CFR 1.17(e), was filed in this application after final rejection. Since this application is eligible for continued examination under 37 CFR 1.114, and the fee set forth in 37 CFR 1.17(e) has been timely paid, the finality of the previous Office action has been withdrawn pursuant to 37 CFR 1.114. Applicants' submission, filed 8/13/07 and 9/13/07, has been entered.

Amended claims 1, 3, 8, 13, 14, and 17, filed 9/13/07, are acknowledged. Claims 4-7, 10-12, 15-16, and 18-19 remain withdrawn due to being drawn to non-elected Groups.

Claims herein under examination are 1-3, 8-9, 13-14, and 17.

Claim Rejections - 35 USC § 112, Second paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-3, 8-9, 13-14, and 17 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 1 (lines 4-5), 8 (lines 5-6), 13 (lines 8-9), and 17 (lines 6-7) recite "generating complementary sequence data from a probe nucleotide sequence that may be bound to a target nucleotide sequence", "generating complementary sequence data from the probe nucleotide sequence that may be bound to a target nucleotide sequence", or "generate complementary sequence data from the probe nucleotide sequence that may be bound to a target nucleotide

sequence" which is confusing. It is unclear if the "complementary sequence data" is complementary to the probe or to the target nucleotide sequence. It is unclear if the limitation "that may be bound to a target nucleotide sequence" is referring to the "complementary sequence data" or to the "probe nucleotide sequence". Clarification of this issue via clearer claim wording is requested. Claims 2-3, 9, and 14 are also rejected due to their dependency from claims 1, 8, and 13.

Claim Rejections – 35 USC §102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1-3, 8-9, 13-14, and 17 are rejected under 35 U.S.C. 102(b) as being anticipated by Fujimiya et al. (P/N 5,706,498).

Fujimiya et al. disclose a computer system, method, program, and computer readable medium for executable screening nucleotide sequences (abstract and Figures 2-4, col. 3, second paragraph, col. 8, first 2 paragraphs; and col. 13, first paragraph), as stated in the preamble of instant claims 1, 8, 13, and 17. Fujimiya et al. disclose storing sequence data of genes including target sequence data and key sequence data which exhibit a high degree of similarity (abstract and title and Figure 2 and col. 1, third paragraph; col. 2, fourth paragraph; col. 9, last paragraph) for homology retrieval (col. 2, fourth paragraph) including key memory and target memory

(Figure 2) which represent a target and a complementary sequence data storing units, as stated in instant claims 1, 8, 13, and 17. Fujimiya et al. disclose retrieval databases and analyzing and determining the final sequence of bases by extracting a portion of the gene probe bound to a chromosome (col. 2, third paragraph) which represents generating complementary sequence data from a probe sequence that may be bound to the target sequence and storing such data, as stated in instant claims 1, 8, 13, and 17. Fujimiya et al. disclose a dynamic operation unit for determining the degree of similarity between the target data and the key data by utilizing base sequence data of each (abstract), grouping homologous sequences, and retrieving the homologous gene sequence (col. 1, fifth paragraph and col. 2, second paragraph) using dynamic programming by summing up points from the starting point of the operation for determining the locally optimal path (i.e. number of adjustments) solution as a whole using insertions, deletions, and substitutions for the first to last combinations of data (col. 2, last paragraph, col. 3, third and fourth paragraphs, and Figures 7a and 7b), altering target data one after another with respect to key data and determining degree of similarity by entering the base sequence data one after another of the target data and storing the maximal sum value occurring at the time of operation (col. 9, lines 21-67; col. 12, lines 32-39; col. 13, lines 1-22), as well as displaying maximal values of each target data in the order of higher degrees of similarity (col. 23, third paragraph) and probe binding evaluation (col. 2, second and third paragraphs) which represents an evaluation processing unit for evaluating a binding possibility of the target nucleotide sequence data to the complementary sequence data via determination of whether the complementary sequence data is similar to a subsequence of the target nucleotide sequence data in descending order of edit distance of binding precision, wherein edit distance is the number of times

nucleotide characters of the subsequence are required to be adjusted to generate the complementary (key) sequence data, as stated in instant claims 1, 8, 13, and 17. Fujimiya et al. disclose preparing a gene probe on the basis of the gene having high retrieval accuracy and analyzing and determining the binding possibility of the probe on the involved gene on a chromosome (col. 2, second and third paragraphs), as stated in instant claims 1, 8, 13, and 17. Fujimiya et al. disclose a database and retrieving of sequence data using a sequence similar thereto (col. 1, first paragraph) and probe binding analysis and determination (col. 2, second and third paragraphs) and evaluation processing for a user (col. 23, third paragraph) which represents a storage unit for storing the evaluation result for the user in determining probe binding effectiveness and reliability, as stated in instant claims 1, 8, 13, and 17. Fujimiya et al. disclose using 10 base elements in the sequence data (col. 4, second paragraph) as well as using partial sequences (col. 4, third paragraph). Fujimiya et al. disclose a system including storage of data and a similarity degree whereby the score value at the initial condition is set to zero given the condition in which the maximal length α of the sequence is inserted or lost at one time involving partial sequences as well as setting α to 1 to get a maximal score value (col. 4, last paragraph, and col. 5, and abstract) and performing an operation until reaching a predetermined length of the key or target data and acquiring the maximal value of the sum values with direction selection data (col. 10, line 57 to col. 11, line 43) as well as a constant value to compare sum values (col. 12, lines 1-17) which represents a maximum edit distance storing unit, as stated in instant claims 2, 8, 13, and 17. Fujimiya et al. disclose setting a maximal value as a score of the node and applied to the origin and subsequent lattice points until finishing the basic operation and determining the wholly optimal disposition of the three routes (col. 5, last paragraph to col. 6,

second paragraph) which represents determining a termination point and a termination-determining unit determining evaluation carried out over maximal (acceptable) edit distance, as stated in instant claims 3, 9, and 14. Fujimiya et al. disclose a score value of each route is added, including target-side data and key-side data, as well as outputting sequence data and displaying maximal values and direction selection data (path) (col. 3, third to col. 4, first paragraph; col. 5, second to last paragraph to col. 6, second paragraph; col. 10; col. 11, lines 44-48; col. 20, first paragraph; col. 23, third paragraph; and Figures 7 and 8) which represents reading out each target nucleotide sequence data, complementary sequence data, and each maximum acceptable edit distance, as stated in instant claims 8, 13, and 17. Fujimiya et al. disclose the wholly optimal disposition is determined after the basic operations have been made (col. 6, second paragraph and Figures 3-4 and 6) and an interruption signal issued to the microprocessor when the operation is terminated (col. 24, last paragraph) which represents generating a termination signal in response to the determination result, as stated in instant claims 9 and 14. Fujimiya et al. disclose using the ability to apply dynamic programming to a local region having approximately 16 bases (col. 7, fourth paragraph).

Thus, Fujimiya et al. anticipate the instant invention.

Applicant summarizes Fujimiya et al. and argues that Fujimiya et al. fail to disclose the evaluation processing unit or step, as recited in independent claims 1, 8, 13 and 17. This statement is found unpersuasive as Fujimiya et al. disclose a dynamic operation unit for determining the degree of similarity between the target data and the key data by utilizing base sequence data of each (abstract), grouping homologous sequences, and retrieving the

homologous gene sequence (col. 1, fifth paragraph and col. 2, second paragraph) using dynamic programming for determining the locally optimal path (i.e. number of adjustments) solution as a whole using insertions, deletions, and substitutions for the first to last combinations of data (col. 2, last paragraph, col. 3, third and fourth paragraphs, and Figures 7a and 7b), altering target data one after another with respect to key data and determining degree of similarity by entering the base sequence data one after another of the target data and storing the maximal sum value occurring at the time of operation (col. 9, lines 21-67; col. 12, lines 32-39; col. 13, lines 1-22), as well as displaying maximal values of each target data in the order of higher degrees of similarity (col. 23, third paragraph) and probe binding evaluation (col. 2, second and third paragraphs) which represents an evaluation processing unit for evaluating a binding possibility of the target nucleotide sequence data to the complementary sequence data via determination of whether the complementary sequence data is similar to a subsequence of the target nucleotide sequence data in descending order of edit distance of binding precision, wherein edit distance is the number of times nucleotide characters of the subsequence are required to be adjusted to generate the complementary (key) sequence data.

Applicant further argues that Fujimiya et al. fail to disclose the storing of a maximum acceptable edit distance of binding precision between a target nucleotide sequence and a probe nucleotide sequence, as recited in independent claims 8, 13 and 17. This statement is found unpersuasive as Fujimiya et al. disclose a system including storage of data and a similarity degree whereby the score value at the initial condition is set to zero given the condition in which the maximal length α of the sequence is inserted or lost at one time involving partial sequences as well as setting α to 1 to get a maximal score value (col. 4, last paragraph, and col. 5, and

abstract) and performing an operation until reaching a predetermined length of the key or target data and acquiring the maximal value of the sum values with direction selection data (col. 10, line 57 to col. 11, line 43) as well as a constant value to compare (and possibly replace) sum values (col. 12, lines 1-17) which represents a maximum acceptable edit distance storing unit, as stated in instant claims 2, 8, 13, and 17. Fujimiya et al. disclose setting a maximal value as a score of the node and applied to the origin and subsequent lattice points until finishing the basic operation and determining the wholly optimal disposition of the three routes (col. 5, last paragraph to col. 6, second paragraph) which represents determining a termination point and a termination-determining unit determining evaluation carried out over maximal (acceptable) edit distance. Applicant's arguments are deemed unpersuasive for the reasons given above.

Conclusion

No claim is allowed.

Papers related to this application may be submitted to Technical Center 1600 by facsimile transmission. Papers should be faxed to Technical Center 1600 via the PTO Fax Center. The faxing of such papers must conform to the notices published in the Official Gazette, 1096 OG 30 (November 15, 1988), 1156 OG 61 (November 16, 1993), and 1157 OG 94 (December 28, 1993) (See 37 CFR §1.6(d)). The Central Fax Center number for official correspondence is (571) 273-8300.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Carolyn Smith, whose telephone number is (571) 272-0721. The examiner can normally be reached Monday through Thursday from 8 A.M. to 6:30 P.M.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Marjorie Moran, can be reached on (571) 272-0720.

November 1, 2007

/Carolyn Smith/
Primary Examiner
AU 1631